

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 4, 2002, 07:39:00 ; Search time 25.94 Seconds  
(without alignments)  
3404.244 Million cell updates/sec

Title: US-08-153-397A-2

Sequence: 1 MGPEALSSLLLLLVASGDA.....QRPPSQLHRLAEADALNTV 919

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4881	99.0	913	2	receptor tyrosine
2	4656.5	94.5	876	2	protein-tyrosine k
3	4576.5	92.9	910	2	tyrosine kinase re
4	2404	48.8	855	2	protein-tyrosine k
5	2341	47.5	819	2	tyro 10 receptor k
6	1159	23.5	220	2	receptor tyrosine
7	969	19.7	791	2	hypothetical prote
8	963	19.5	248	2	receptor tyrosine
9	929.5	18.9	183	2	receptor tyrosine
10	648.5	13.2	821	1	brain-derived neur
11	648.5	13.2	821	1	brain-derived neur
12	648	13.1	818	1	brain-derived neur
13	645	13.1	818	1	brain-derived neur
14	641.5	13.0	825	2	brain-derived neur
15	640.5	13.0	825	2	brain-derived neur
16	628	12.7	790	1	nerve growth facto
17	624.5	12.7	825	1	neurotrophin-3 rec
18	623.5	12.7	839	1	neurotrophin-3 rec
19	615	12.5	503	4	hypothetical TPR/T
20	613.5	12.4	803	1	neurotrophin-3 rec
21	608	12.3	282	2	brain-derived neur
22	608	12.3	806	2	hypothetical prote
23	604	12.3	852	2	tyrosine kinase C
24	597.5	12.1	946	1	for-related recept
25	597	12.1	737	2	hypothetical prote
26	590.5	12.0	605	2	protein-tyrosine k
27	590	12.0	871	1	protein-tyrosine k
28	588.5	11.9	881	1	protein-tyrosine k
29	584	11.9	685	1	neurotrophic recep

30	576	11.7	981	1	FOATGM	gag-ab1 polyprotel
31	571	11.6	737	2	T31349	hypothetical prote
32	540.5	11.0	1363	2	T43320	insulin-like growt
33	537	10.9	937	2	A45082	neurotrophic recep
34	535.5	10.9	1382	1	INHUR	insulin receptor p
35	532.5	10.8	402	1	TYEVUR	insulin receptor p
36	531.5	10.8	1372	2	A34157	insulin receptor p
37	528.5	10.7	1383	2	A36080	insulin receptor p
38	523	10.6	1520	1	TVFPA	insulin receptor p
39	522.5	10.6	2338	2	T73957	protein-tyrosine k
40	522	10.6	2347	1	TYVHRS	kinase-related pro
41	521.5	10.6	2311	1	TYVHRS	kinase-related pro
42	520	10.6	1123	2	A39962	kinase-related tra
43	518	10.5	2340	2	I48310	kinase-related pro
44	517	10.5	1130	1	TVHUA	protein-tyrosine k
45	517	10.5	1300	2	A36502	insulin receptor-r

## ALIGNMENTS

RESULT 1  
A48280  
receptor tyrosine kinase - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 24-Sep-1999  
R:Johnson, J.D.; Edman, J.C.; Rutter, W.J.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681, 1993  
A:Title: A receptor tyrosine kinase found in breast carcinoma cells has an extracell.  
A:Reference number: A48280; MUID:93296201  
A:Accession: A48280  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-913 <RES>  
A:Cross-references: GB:L11315; NID:9403386; PID:AAA02866.1; PID:9403387  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino  
C:Keywords: ATP  
F:30-185/Domain: discoidin I amino-terminal homology <DNI>  
F:608-912/Domain: protein kinase homology <KIN>  
F:616-624/Region: protein kinase ATP-binding motif

Query Match	99.0%;	Score 4881;	DB 2;	Length 913;
Best Local Similarity	99.1%;	Pred. No. 5.8e-214;		
Matches 911;	Conservative	2;	Mismatches 0;	Indels 6;
				Gaps 1;
QY	1	MGPEALSSLLLLLVASGDA	DMKGFDPKCRVALGMDRTIPDSDISASSMSDSTAR	60
DB	1	MGPEALSSLLLLLVASGDA	DMKGFDPKCRVALGMDRTIPDSDISASSMSDSTAR	60
QY	61	HSRLSSDDGDMCPAGSVFPEKEEYLDQRLHLVALYVQGNHAGLGAEFRSRL	120	
DB	61	HSRLSSDDGDMCPAGSVFPEKEEYLDQRLHLVALYVQGNHAGLGAEFRSRL	120	
QY	121	RYSRDGRMMGKDMWGOEIVSGNDEPGVYLKDGPPVARTLVFYPRADEVMSCLRV	180	
DB	121	RYSRDGRMMGKDMWGOEIVSGNDEPGVYLKDGPPVARTLVFYPRADEVMSCLRV	180	
QY	121	RYSRDGRMMGKDMWGOEIVSGNDEPGVYLKDGPPVARTLVFYPRADEVMSCLRV	180	
DB	121	RYSRDGRMMGKDMWGOEIVSGNDEPGVYLKDGPPVARTLVFYPRADEVMSCLRV	180	
QY	181	ELYGLMRDGLISTYAPVQGYTISEAVYLANDSTYDGHVGGLOYGGLQGLADGVGDD	240	
DB	181	ELYGLMRDGLISTYAPVQGYTISEAVYLANDSTYDGHVGGLOYGGLQGLADGVGDD	240	
QY	241	FKKSELVWPGDYDVGSMNSFSGTYEMEFERLALFAQMYCHNNMTTLGARLPFG	300	
DB	241	FKKSELVWPGDYDVGSMNSFSGTYEMEFERLALFAQMYCHNNMTTLGARLPFG	300	
QY	301	VECRFRGPPAMAEGERPHNLGNIADPPARAVSVPLGGRVARTLOCRTFAPPWILFS	360	
DB	301	VECRFRGPPAMAEGERPHNLGNIADPPARAVSVPLGGRVARTLOCRTFAPPWILFS	360	
QY	361	ELSFSDVYVNNSSPALGCTPPAPWMPGPPPTNFSLELPRGOQPVAKAGSPTAILI	420	
DB	361	ELSFSDVYVNNSSPALGCTPPAPWMPGPPPTNFSLELPRGOQPVAKAGSPTAILI	420	

D	b	361	EISISDVNNSSBALGTFEPAPAMWPPGPPTNFSSLELEPRGQOPVAKAESGP	TAII	420
Q	y	421	GCLVAIIILLILLITALLMLKRLHMRRLLSKAEKRVLEELTVHNSVGD	TLINNRGPR	480
D	b	421	GCLVAIIILLILLITALLMLKRLHMRRLLSKAEKRVLEELTVHNSVGD	TLINNRGPR	480
Q	y	481	PPVQEBRPRGNPNHSAFCVNSGALLNSPAYRLLATARP	PRGGRPTMAKPTN	540
D	b	481	PPVQEBRPRGNPNHSAFCVNSGALLNSPAYRLLATARP	PRGGRPTMAKPTN	540
Q	y	541	QAYSGDVMEPEKPCAPLPPRPPONSYPHYAEADIVTLQGTGGNTYAV	PLPPGAGDGP	600
D	b	541	QAYSGDVMEPEKPCAPLPPRPPONSYPHYAEADIVTLQGTGGNTYAV	PLPPGAGDGP	600
Q	y	601	PRVDPFRSLRFEKKEKGEGFGEVHLCEVDSPDVLSDPLNVRKGNPL	LLVAVKILRPD	660
D	b	601	PRVDPFRSLRFEKKEKGEGFGEVHLCEVDSPDVLSDPLNVRKGNPL	LLVAVKILRPD	660
Q	y	661	ATKNASSLSESRNDFLEKVINMSRLDPNIIIRLLGCVODDPLCMITD	YENKNDLQOFLS	720
D	b	661	ATKNA-----RNDFLKEVKIMSRLDPNIIIRLLGCVODDPLCMITD	YENKNDLQOFLS	714
Q	y	721	AHOEDRAEAGAPDGGAAOGPTISYPMLLHYAAQJASGMYRATATNF	VRDADRNCU	780
D	b	715	AHOEDRAEAGAPDGGAAOGPTISYPMLLHYAAQJASGMYRATATNF	VRDADRNCU	774
Q	y	781	GENFTIKIADFGMSRNLVADITYRVQRAVLP	IRMMAMECILLGKFTTASDVNAFGVTLM	840
D	b	775	GENFTIKIADFGMSRNLVADITYRVQRAVLP	IRMMAMECILLGKFTTASDVNAFGVTLM	834
Q	y	841	EYLMCLCAOGPGQUTDQVLENAAGEFFRQDGRQVYLSRPACQGL	EYLMCLCWSRESD	900
D	b	835	EYLMCLCAOGPGQUTDQVLENAAGEFFRQDGRQVYLSRPACQGL	EYLMCLCWSRESD	894
Q	y	901	RPPESOLHRFLAEDALNTV	919	
D	b	895	RPPESOLHRFLAEDALNTV	913	

RESULT 2

A49508

protein-tyrosine kinase (EC 2.7.1.112) trkE precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 04-Feb-2000

C:Accession: A49508, I38358, S57402

R:Di\_Marco, E.; Cuttuli, N.; Guerra, L.; Cancedda, R.; De Luca, M.

J. Biol. Chem. 268, 24290-24293, 1993

A:Title: Molecular cloning of trkE, a novel trk-related putative tyrosine kinase receptor

A:Reference number: A49508; MUID:94043265

A:Accession: A49508

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-876 <DRA>

A:Cross-references: EMBL:X74979; NID:G400463; PIDD:CA52915.1; PIDD:G400463

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-terminal domain; ATP, phosphotransferase, tyrosine-specific protein kinase

F:30315/Domain: discoidin I amino-terminal homology <kin>

F:531-875/Domain: discoidin I amino-terminal homology <DNA>

F:579-587/Region: protein kinase ATP-binding motif

Query Match	94.5%	Score 4656.5;	DB 2;	Length 876;
Best Local Similarity	95.3%	Pred. NO. 8.1e-204;		
Matches 876; Conservative	0;	Mismatches 0;	Indels 43;	Gaps 2;

QY	1	MGPAALSSLLILLVAVSGDDMDMGHFPACRCALGQMDPTIPDSISASSMSDSTAA	60
Db	1	MGPAALSSLLILLVAVSGDDMDMGHFPACRCALGQMDPTIPDSISASSMSDSTAA	60
QY	61	HSRRLESDGGANCPASVYPRKEEYQYDVLRLHVAIVGTGGRNAGGIGKEFSRYRL	120
Db	61	HSRRLESDGGANCPASVYPRKEEYQYDVLRLHVAIVGTGGRNAGGIGKEFSRYRL	120

QY	121	FRSQRGRMMCKDMSGEVIGSNGEDPEGVYLKDLGPPMVARLRYEYPRADRWASVCLRY	180
Db	121	FRSQRGRMMCKDMSGEVIGSNGEDPEGVYLKDLGPPMVARLRYEYPRADRWASVCLRY	180
QY	161	ELYGCLMRDGLLSYAPVGGTQMTYLSAEAVYLLDSTYDGHGTGGLGYGGLADGVGDD	240
Db	161	ELYGCLMRDGLLSYAPVGGTQMTYLSAEAVYLLDSTYDGHGTGGLGYGGLADGVGDD	240
QY	241	FRKSOELAVMPGYDVGMSNHSFSSGYIEMEPEDRLAFOAMOVHCNNMHTLGARLPGC	300
Db	241	FRKSOELAVMPGYDVGMSNHSFSSGYIEMEPEDRLAFOAMOVHCNNMHTLGARLPGC	300
QY	301	VECRRRGPPAAMAGEEPNRHNLGGLGDPRAARAVSPLGGVAVRFLQCRFLFAGPMLIFS	360
Db	301	VECRRRGPPAAMAGEEPNRHNLGGLGDPRAARAVSPLGGVAVRFLQCRFLFAGPMLIFS	360
QY	361	EISFISIDVYNNSSPALGTFPPAPMWPMPPEPTNFSLSLELPRGOOPAPAKEGSPAILI	420
Db	361	EISFISIDVYNNSSPALGTFPPAPMWPMPPEPTNFSLSLELPRGOOPAPAKEGSPAILI	420
QY	421	GCLVAIIIIIIIIITATMLMRLLMRLLSKARRVLEELTYHLSVPGDTIINNRPGRRE	480
Db	421	GCLVAIIIIIIIIITATMLMRLLMRLLSKARRVLEELTYHLSVPGDTIINNRPGRRE	480
QY	481	PPPYOEPAPRGNPNPSAPACVNGSALLLSNPAYRLLATYARPPRGPPPTPAKAKPTNT	540
Db	481	PPPYOEPAPRGNPNPSAPACVNGSALLLSNPAYRLLATYARPPRGPPPTPAKAKPTNT	540
QY	541	QAYSDDIYEPKPCGAPLLPPPPONSVPHYAEADITYTLOGTGGNTYAVPALPPEAVGDGP	600
Db	505	-AYSQDYMEPRKPGAPLLPPPPONSVPHYAEADITYTLOGTGGNTYAVPALPPEAVGDGP	563
QY	601	PRVDPFRRLRFEKELGEGGEGEYHLCVDSPODLVSLDFPLNARKGHPLLVAYKILRPD	660
Db	564	PRVDPFRRLRFEKELGEGGEGEYHLCVDSPODLVSLDFPLNARKGHPLLVAYKILRPD	623
QY	661	ATKNASFSLFRNDFLAKVYKIMSRLKDPNIIIRLGVCOVDDPLCMITDYMENGDLNOLS	720
Db	624	ATKNA-----RNDPLKKEVKIMSRLKDPNIIIRLGVCOVDDPLCMITDYMENGDLNOLS	677
QY	721	AHOLEDRAAEAPGDDGOAAGOPTISYPMLLHVAAQIASGMRYLATLNFVHNDLATTRCLV	780
Db	678	AHOLEDRAAEAPGDDGOAAGOPTISYPMLLHVAAQIASGMRYLATLNFVHNDLATTRCLV	737
QY	781	GENFTIKIADGMSRNLVAGDYRYVQGRAVLPIRMAMECILMKRFTTASDYVAFFCTLM	840
Db	738	GENFTIKIADGMSRNLVAGDYRYVQGRAVLPIRMAMECILMKRFTTASDYVAFFCTLM	797
QY	841	EVLMLCRAOPFGQLTDEOVIEENAGEFFRDOGRUYLSHPACPOGLYELMLRCMSRESEQ	900
Db	798	EVLMLCRAOPFGQLTDEOVIEENAGEFFRDOGRUYLSHPACPOGLYELMLRCMSRESEQ	857
QY	901	RPFSQULHRFLAEDALNTV 919	
Db	858	RPFSQULHRFLAEDALNTV 876	

RESULT 3  
A:53137  
tyrosine kinase receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999  
C:Accession: A53137  
R:Sanchez, M.P.; Tapley, P.; Saint, S.S.; He, B.; Pulido, D.; Barbacid, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 1819-1823, 1994  
A:Title: Multiple tyrosine protein kinases in rat hippocampal neurons: Isolation of P  
A:Reference number: A53137; MUID:94173920  
A:Accession: A53137  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-910 <RES>  
A:Cross-references: GB:L26525; NID:q432480; PIDN:AAA21089.1; PID:q432481  
A:Genetics:

A;Gene: Ptk-3  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter  
C;Keywords: ATP  
F;31-186/Domain: discoidin I amino-terminal homology <DNI>  
F;605-909/Domain: protein kinase homology <KIN>  
F;613-621/Region: protein kinase ATP-binding motif

Query Match 92.9%; Score 4576.5; DB 2; Length 910;  
Best Local Similarity 93.0%; Pred. No. 3.5e-200;  
Matches 856; Conservative 20; Mismatches 33; Indels 11; Gaps 3;

1 MGPEALSS-LLILLVAGSDADMGKHPDPAKCRATGMDRTIPDSISASSWSSTAA 59  
1 MGTGLSSLLILLVLTIGDADMGKHPDPAKCRATGMDRTIPDSISASSWSSTAA 60  
60 RHRLSSSDGDMCPAGSVFPEEYLOVDLRLHLVALVGTQGRHAGLGKFEFSR 119  
61 RHRLSSSDGDMCPAGSVFPEEYLOVDLRLHLVALVGTQGRHAGLGKFEFSR 120  
120 LRSRDGRMGKMDKMGQVITSGNDEPQVYAKDGPVAVARVRYPRADRYMSYCLR 179  
121 LRSRDGRMGKMDKMGQVITSGNDEPQVYAKDGPVAVARVRYPRADRYMSYCLR 180  
180 VELYGCLMRDGLSTYAPVQTYLSEAYVLYNDSTYDGHVGTGGLQGLADGVVGLD 239  
181 VELYGCLMRDGLSTYAPVQTYLSEAYVLYNDSTYDGHVGTGGLQGLADGVVGLD 240  
240 DRRKSOELRWPGDYVYGNSSFSGGYVMEFEFDRLRAFOAMOVHNNMTLGARLP 299  
241 DRRKSOELRWPGDYVYGNSSFSGGYVMEFEFDRLRAFOAMOVHNNMTLGARLP 300  
300 GVECRRRRGPAMAMEGEPHNNHNGNLGDPRAAVSVPLGGRVAFRLQCFLEAGPMLF 359  
301 GVECRRRRGPAMAMEGEPHNNHNGNLGDPRAAVSVPLGGRVAFRLQCFLEAGPMLF 360  
360 SEISFISDVNNSSPALGTFPPAPMPGPPTNFSLELEPRGQPVAKAGSPATL 419  
361 SEISFISDVNNSSPALGTFPPAPMPGPPTNFSLELEPRGQPVAKAGSPATL 416  
420 TCGCLVAIILLLIILMLRLHMRRLSKAERRVLEELTVHLVSPGDTILINNRPGR 479  
421 TCGCLVAIILLLIILMLRLHMRRLSKAERRVLEELTVHLVSPGDTILINNRPGR 476  
480 EPPPOEPRRGNPHSACVNGSALLSNPARYLLLTATYARPPGPPPPAMAKPTN 539  
477 EPPPOEPRRGNPHSACVNGSALLSNPARYLLLTATYARPPGPPPPAMAKPTN 536  
540 TQAVSGDYMEPEKPGAPLPPPPONSVPYAEADIVTLGGVYGGNTYAVPALPGAVDG 599  
537 TQAGSGDYMEPEKPGAPLPPPPONSVPYAEADIVTLGGVYGGNTYAVPALPGAVDG 596  
600 PPRVDFPNSRLRFKKEKLGEGFGEVHLCEVDSPLDFLNNKRGHLLVAVKILRP 659  
597 PPRVDFPNSRLRFKKEKLGEGFGEVHLCEVDSPLDFLNNKRGHLLVAVKILRP 656  
660 DATKASSLFERNDELKVKIMSLKPNITRLGLVCYQDDPLCITITYMENGDIHQPL 719  
657 DATKASSLFERNDELKVKIMSLKPNITRLGLVCYQDDPLCITITYMENGDIHQPL 710  
720 SAHOLEDRKAAGPDGGAAGPTISYPMILHVAQAQIASGMRYLATLNVHDLATRNCL 779  
721 SAHOLEDRKAAGPDGGAAGPTISYPMILHVAQAQIASGMRYLATLNVHDLATRNCL 770  
780 VGENTTIIRIAFGMSRNLYAGDYVVOGRAVLPIRMAMECILMKFTTASDVMAFGVTL 839  
771 VGENTTIIRIAFGMSRNLYAGDYVVOGRAVLPIRMAMECILMKFTTASDVMAFGVTL 830  
840 MEVLMLCAOPRGOLTDGOVITENAGEFFRDGROYVLSRPPACPGGLYVLMRCSRSSE 899  
831 MEVLMLCAOPRGOLTDGOVITENAGEFFRDGROYVLSRPPACPGGLYVLMRCSRSSE 890  
900 QRPFSQHLRLFLADALNTV 919

Db 891 QRPFSQHLRLFLADALNTV 910

RESULT 4  
542621  
protein-tyrosine kinase (EC 2.7.1.112) - human

C;Species: Homo sapiens (man)  
C;Date: 07-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 24-Sep-1999  
C;Accession: S42621  
R;Kern, T.; Holtrich, U.; Braeuninger, A.; Boehme, B.; Wolf, G.; Ruebsaamen-Walzgmann, Oncogene 8, 3433-3440, 1993  
A;Title: Structure, expression and chromosomal mapping of TRK from man and mouse: a  
A;Reference number: S42621; M0ID:94067796  
A;Accession: S42621  
A;Molecule type: mRNA  
A;Residues: 1-855 <KAR>  
A;Cross-references: EMBL:X74764; NID:q433337; PIDN:CA45277.1; PID:q433338  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino  
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase  
F;29-185/Domain: discoidin I amino-terminal homology <DNI>  
F;561-855/Domain: protein kinase homology <KIN>  
F;569-577/Region: protein kinase ATP-binding motif

Query Match 48.8%; Score 2404; DB 2; Length 855;  
Best Local Similarity 51.8%; Pred. No. 6.8e-102;  
Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

3 PEALSSLLILLVAGSDADMGKHPDPAKCRATGMDRTIPDSISASSWSSTAA 62  
5 PRLVLFLLPLTIS--SAKAQVNPALICRYPGMSGGQIPDDITASSQWSESTAAKYG 61  
63 RLESSDGDGAMCPAGSVFPEEYLOVDLRLHLVALVGTQGRHAGLGKFEFSR 121  
62 RLESSDGDGAMCPAGSVFPEEYLOVDLRLHLVALVGTQGRHAGLGKFEFSR 121  
122 YSRDGRMGKMDKMGQVITSGNDEPQVYAKDGPVAVARVRYPRADRYMSYCLR 181  
122 YSRDGRMGKMDKMGQVITSGNDEPQVYAKDGPVAVARVRYPRADRYMSYCLR 181  
182 YSGCLMRDGLSTYAPVQTYLSEAYVLYNDSTYDGHVGTGGLQGLADGVVGLD 239  
182 YSGCLMRDGLSTYAPVQTYLSEAYVLYNDSTYDGHVGTGGLQGLADGVVGLD 239  
240 DRRKSOELRWPGDYVYGNSSFSGGYVMEFEFDRLRAFOAMOVHNNMTLGARLP 299  
241 DRRKSOELRWPGDYVYGNSSFSGGYVMEFEFDRLRAFOAMOVHNNMTLGARLP 299  
300 GVECRRRRGPAMAMEGEPHNNHNGNLGDPRAAVSVPLGGRVAFRLQCFLEAGPMLF 359  
301 GVECRRRRGPAMAMEGEPHNNHNGNLGDPRAAVSVPLGGRVAFRLQCFLEAGPMLF 359  
360 SEISFISDVNNSSPALGTFPPAPMPGPPTNFSLELEPRGQPVAKAGSPATL 419  
360 SEISFISDVNNSSPALGTFPPAPMPGPPTNFSLELEPRGQPVAKAGSPATL 418  
360 SEISFISDVNNSSPALGTFPPAPMPGPPTNFSLELEPRGQPVAKAGSPATL 418  
419 TCGCLVAIILLLIILMLRLHMRRLSKAERRVLEELTVHLVSPGDTILINNRPGR 476  
401 TCGCLVAIILLLIILMLRLHMRRLSKAERRVLEELTVHLVSPGDTILINNRPGR 476  
477 GPREP-----PPVDFPNSRLRFKKEKLGEGFGEVHLCEVDSPLDFLNNKRGHLLVAVKILRP 523  
461 SPESDGSNSTYDRIPLRPDYQEP-----SLIKRLPEF----- 494  
524 PRGPPPPAMAKPTNTQAVSGDYMEPEKPGAPLPPPPONSVPYAEADIVTLGGVYGG 583  
495 -----APEEESGSGGVKVPVQSGP-----EGVPHYAADIVNLGGVYGG 535  
584 NTYAVPALPGAVGDPGRPV--DFPRSRRLRFKKEKLGEGFGEVHLCEVDSPLDFL 642  
536 NTYAVPALPGAVGDPGRPV--DFPRSRRLRFKKEKLGEGFGEVHLCEVDSPLDFL 595

QY 643 NVKRGHPLLVAVKILRPATKNASPSLESRNDFLKEVKIMSRDKDPNITLLGCVQDDP 702  
 Db 536 DVSANQPLVAVKMLRPADKNA-----RNDPLKEIKIMSRDKDPNITLLGCVQDDP 649  
 QY 703 LCMITDVWENGLNOFLSAHOLEDKAAGPDDQAAGPISYPMILHVAQAASGRY 762  
 Db 650 LCMITEHENDLNOFLSRHE-----PPNSSSDVRTVSTNLEKMTQASGMY 700  
 QY 763 LATINEFVARDLATNCLVGENFTIKIADFGMSRLYAGDYRVQRAVLPIRMAMECIL 822  
 Db 701 LSLINFEVARDLATNCLVGYKNYTIKIDFGMSRLYSGDIYRIGRAVLPIRMAMECIL 760  
 QY 823 MGFRTASDVAFVGYTLMEVLMCLRAOPFGQITDQVYENAGFEPRDQGVYLSRPPAC 882  
 Db 761 LKFTFADSVAFVGYTLMEFTFCQCEPQYQSLSDEQVIENTGEFFRDQGVYLSRPPAC 820  
 QY 883 POGLEYMLRCMSRESEORPPFQSLHRLAE 913  
 Db 821 PDSYKMLSCMRDRTKNRPSFOETHILLLO 851

## RESULT 5

tyro 10 receptor kinase - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence,revision 02-Jul-1996 #text\_change 24-Sep-1999  
 C:Accession: I48859; S42796  
 R:lat, C.; Lemke, G.  
 Oncogene 9, 877-883, 1994  
 A:Title: Structure and expression of the Tyro 10 receptor tyrosine kinase.  
 A:Reference number: I48859; MUID:94151011  
 A:Accession: I48859  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-819 <RES>  
 A:Cross-references: EMBL:X76505; MID:9435161; PIDN:CAA54040.1; PID:9435162  
 C:Genetics:  
 A:Gene: tyro 10  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
 C:Keywords: ATP  
 F:536-819/Domain: protein kinase homology <kin>  
 F:534-542/Region: protein kinase ATP-binding motif

Query Match 47.5%; Score 2341; DB 2; Length 819;  
 Best Local Similarity 52.1%; Pred. No. 46e-99;  
 Matches 465; Conservative 116; Mismatches 208; Indels 104; Gaps 15;

QY 42 IPDSDISASSWSNSTARSHLESSSDGAMCPAGSVFPKE-BEYLQVLDQLRLHVALY 100  
 Db 6 IPDEDITASSQMSSESTAKYGRLDSEEGDAMCPDPIPVQDDLEKFIQIDRLHFTLV 65  
 QY 101 GTGRRHGGGKKEFSRSLRLKYSRDRRMKMRMGQEVISGNEDEBGVYLKLGPPMV 160  
 Db 66 GTGRRHGGGKKEFSRSLRLKYSRDRRMKMRMGQEVISGNEDEBGVYLKLGPPMV 125  
 QY 161 ALRVFETPRADRVASVCLRLVELYCLMRDGLSTAPVQGMVY--SEAVYLDNSTDGH 218  
 Db 126 ARFRLRLPYVDHSMNVCMRVELYGCVMLDGLVSTNAPAGQGFVLPQGSITILLNDSTVDG- 184  
 QY 219 TVGGLQYGGGLQGLADGVVGLDDFRKSOELRLVWPQYDYVGNMNSHSSSGYVMEFEFRLR 278  
 Db 185 AVGYSMTGEGLDGLDGVSGLDLDFQTHYHYWPGDYVGNMNSATNGFLEIMEFRRIR 244  
 QY 279 AFQAMOVHCHNMHTLGLARLPBGVCCRFRGPMAMEGEPARHNLGMLGDPRAAAYVPL 338  
 Db 245 NPTMKVHCHNMHTLGLARLPBGVCCRFRGPMAMEGEPARHNLGMLGDPRAAAYVPL 303  
 QY 339 GGRVAFRLQCFRLFAGPMLIFSEISFISD--VYNNSSPALGCTPPAPWMPGPPPTNFS 396  
 Db 304 HHRVASAIKQCYHFRADNMWSESEITFOSDAMYNNS-----GALPTP----- 346  
 QY 397 SLELEPGQGPVAKAESPTAILIGCLVAITLLILLIALLMLRLHWRLLSKAERYLE 456

Db 347 --NAPTYDPMELKYDSDNTRILLIGCLVAITILLIALLMLRLHWRLLSKAERYLE 403  
 QY 457 EELFVHLSVPGDITLINNR-----GPRREP-----PPYOEPRRGPRPSACVP 501  
 Db 404 DENTVSLSPSESSMFNNRSSSPSEDSNSTYRIRPELRDYOEP----- 449  
 QY 502 NSGALLSNPARYRLLLATYARPGRPGPPRPMKPTNQASGDYMEPEKPGAPLPP 561  
 Db 450 --SRLIKRLPEF-----APGEESGCGGVKPPAPNPP----- 480  
 QY 562 PONSVPYHAEADIVTLOGVTGNTYAVPALPGAVGGPPRY-DFPSRLRFKEKLEGG 620  
 Db 481 --EGVPHYAEADIVNLOGVTGNTYAVPALMDLSCGVAVEEFPRLIAFKKLEGG 538  
 QY 621 FGEVHLCEVDSPODLVSLDFPLNVRKGHPLLVAKILRPDRTKASLSFRNPFLEVK 680  
 Db 539 FGEVHLCEVDSPODLVSLDFPLNVRKGHPLLVAKILRPDRTKASLSFRNPFLEVK 592  
 QY 681 IMSRLKDPNITIRLLGVCVQDDPLCMITDYEMENGLNOFLSAHOLEDKAAGAPDGOAAQ 740  
 Db 593 IMSRLKDPNITIRLLAVCTEDPLCMITEYEMENGLNOFLSRHEPLSSCSDA----- 644  
 QY 741 GPTISYPMLLHVAQAASGRMYLATLNFVHRDLATNCLVGENFTIKIADFGMSRLYAG 800  
 Db 645 --TVSYANKLFMAQIASGMKYLSSLNFVHRDLATNCLVGYKNYTIKIDFGMSRLYSG 702  
 QY 801 DYRYVOGRAVLPITPMAMECILMKFTTASDVAFVGYTLMEVLMCLRAOPFGQITDQVY 860  
 Db 703 DYRIQGRAVLPITPMAMECILLKFTTASDVAFVGYTLMEFTFCQCEPQYQSLSDEQVY 762  
 QY 861 ENAGEFFRDQGVYLSRPPACPOGLEYMLRCMSRESEORPPFQSLHRLAE 913  
 Db 763 ENTGEFFRDQGVYLSRPPACPOGLEYMLRCMSRESEORPPFQSLHRLAE 815

## RESULT 6

receptor tyrosine kinase - rat (fragment)  
 C:Species: Rattus sp. (rat)  
 C:Date: 02-Aug-1996 #sequence,revision 02-Aug-1996 #text\_change 24-Sep-1999  
 C:Accession: I80329  
 R:Sakuma, S.; Saya, H.; Iijichi, A.; Tojilon, P.J.  
 Radiat. Res. 143, 1-7, 1995  
 A:Title: Radiation induction of the receptor tyrosine kinase gene Ptk-3 in normal rat  
 A:Reference number: I59442; MUID:95320273  
 A:Accession: I80329  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-220 <RES>  
 A:Cross-references: GB:S77585; MID:9557332; PIDN:AAB34728.1; PID:9557333  
 C:Genetics:  
 A:Gene: Ptk-3l  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 23.5%; Score 1159; DB 2; Length 220;  
 Best Local Similarity 98.6%; Pred. No. 4e-46;  
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 404 GQOPVAKAESPTAILIGCLVAITLLIALLMLRLHWRLLSKAERYLEELVHL 463  
 Db 1 GQOPVAKAESPTAILIGCLVAITLLIALLMLRLHWRLLSKAERYLEELVHL 60  
 QY 464 SVPGDITLINNRGPRPPYOEPRRGPNPHSAPCVNPGSALLSNPAYRLLATYARP 523  
 Db 61 SVPGDITLINNRGPRPPYOEPRRGPTHSAPCVNPGSALLSNPAYRLLATYARP 120  
 QY 524 PRGGRPTPMAMPNTNQASGDYMEPEKPGAPLPPRPNVPHYAEADIVTLOGVTG 583  
 Db 121 PRGGRPTPMAMPNTNQASGDYMEPEKPGAPLPPRPNVPHYAEADIVTLOGVTG 180  
 QY 584 NTYAVPALPGAVGGPPRYDFPSRLRFKEKLEGGQFGE 623

Db 181 NTYAVPALPGAVGDPPRVDFPRSLRFRKEKLGEGQGE 220

RESULT 7  
T16031  
hypothetical protein F11D5.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 24-Nov-1999  
C:Accession: T16031

Query Match	19.7%	Score 969;	DB 2;	Length 791;
Best Local Similarity	28.3%	Pred. No. 5.5e-37;		
Matches	254;	Conservative 150;	Mismatches 37;	Indels 184;
				Gaps 31;

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0Y 46 DISASSWSDSTAAH-HSRLESSDGDGAMCPAGSVFFKEEBEYLOVDLQRLHLVALVGTQG 104
Db 34 DLMMLGKMGWNISETIRRTAHOESSGAMCPKNOINSLSKEMWLOISFSDVTIVTIVSTEQ 93
0Y 105 RAAGLGKESRSRYRLRYSRDG--RRWGMKDRMGQOEYISGENDEPGLVLDLGPVAPL 163
Db 94 RFDDGGMEXATAFKIQYWPRLNMAASYKDDPELEITPRANDTEHAKRHHLRAITARR 153
0Y 164 VREYPRADRYMASCLELYELTGLMRDGLLSTYAPVGTMYLSEAVYLYNDSTYDGHVYGL 223
Db 154 IRTVPVNSNTRTCMKEVEFGCPDSDLVFEYVNDQGD---LQSGISYHDSYSGNLANSP 210
0Y 224 QY-GGLGQLEADGVYDGDDEPRKSOELRWMPQYDYVGNMNSHFSGGYMEEPFRLRAFOA 282
Db 211 HLTGIGIKLYDGVGNANFVNH-----HKVYGRNRK--RGNVNLAFEESELRNIG 261
0Y 283 MOYHCNNMHTLGARLPGEVCEFRRGPRAMAMEGEPKRNHIG-----NLGDP-- 330
Db 262 ILIHNSN-----EFKKS-AKAFSSATVLESIGKDFSDTIYHFNNDPETS 306
0Y 331 --ARAVSYPLGGRVARELQCRFLA--GPWLLFESLSEISFDVYN-----NSSPLGCTPP 382
Db 307 EYPRMIRIVNNRIKAVARIKLNFTGDSPLFISEVNFESNMHNIELNDVVY----- 360
0Y 383 APMWPPGPPTNFSSLELPPRGOQPAKAEGSEPTALICLVAIIILLILALMTLRH 442
Db 361 -----PDSYVSFSTEHDG--SMFAIIL--FFEMELIVANIIITLYXRR 403
0Y 443 WRRLLS--KAERVYLEEELVHLSTVGDTIILNNRGPREPPYOEPRRGNPDSA 497
Db 404 EYKVAASSEPSPAKREIL-----LTIDGNIKHH---VSPSTYQYAR----- 442
0Y 498 PCVPNGSALLNSPAYRLLLATYARPPRGGPPTPMAKFTYT--QAVSGDYMEKPG 554
Db 443 ---DNLQNNLIEKMPMSPIISDYABDISVCSDYNA---HTPLLYXIDGER-DIQKNS 493
0Y 555 APLLPPPNQNSYPHAEADIVTLQGTGAGNTAVPALPPGAVGDGPPRVDFPRSRLEKE 614
Db 494 NPL-----SSWAKVSDY-----GEVYCT-TLP-----EIRADKLICVS 525
0Y 615 KLGEQFGEVHLICEVDSPODLVSLDFPLNVKRGHPLVAVKILTRDPAFKNAFSLSLRND 674
Db 526 RIGGGEPEVLDLQLEN-----RK-----VAVKLH-----GISQADEFS 560

```

QY 675 ELKEVKIMSRKLDPNIRILLGVCDPDCMTITMYMENGDLNQFISAHQLEDKAEGAPG 7340  
| : : : : | : : : : | : : : : : :  
Db 561 FHREIRVLGSIKHPNVEVVGCTIQKPIILCIMEWMENGDLSXI----- 6095

735 DGAAGPTISYPMLLHVAQIASGMRATLNFVHRDLATRNCVGENFTIKTADFGMS 794

DB 606 ---LKNPTIQISQCSICQQLAGLAYLESCNFFVHDIARNCNLYDGEQNVKTDFGMA 661

Db 662 RSLYSQSEYKKEGKFLPIRMHAMEALLIGKFTSTASDVWGFGVITMEIFSLCSEKPYSDM 7211

RESULT 8  
A44547  
receptor tyrosine kinase Xtk - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 10-Sep-1997  
#accession: A44547

F;1-246/Domain: protein kinase homology (fragment) <KIN>

Query Match	19.5%	Score 963;	DB 2;	Length 248;
Best Local Similarity	72.6%	Pred. No. 3,36-37;		
Matches 175; Conservative	28;	Mismatches 32;	Indels 6;	Gaps 1;

[illegible]

Db 2 SLISNSDFLKEKILKLSRLSDPHIIRLLGACLDEBPFLCMITEYMEINGDLNDFLSSHHLDEG 61

Db 62 EENG-----AHCLPAISYSSLLHALQICSGKRYLISLNFVHRLDASRNCVIGENLTIK 115

QY 788 IADFGMSBNLYAGDIYRVQGRAVLPIRMMAMECIIMKGKFTTASDVWAFVTILMEVLMICR 847

116 TADFGMSRLYAGDIYRIQGRAVLPIRMMAMECILMGKFTTASDVWSFGVTLWEILMLCK 175

```

RESULT      9
159442      receptor tyrosine kinase - rat (fragment)
C1:Species: Rattus sp. (rat)
C1:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
C1:Accession: 159442
R1:Sakuma, S.; Saya, H.; Ijichi, A.; Tofilon, P. J.
Radiat. Res. 143, 1-7, 1995
A1>Title: Radiation induction of the receptor tyrosine kinase gene Ptk-3 in normal rat
A1:Reference number: 159442; MUID:95320273
A1:Accession: 159442
A1:Status: preliminary; translated from GB/EMBL/DBD
A1:Molecule type: mRNA
A1:Residues: 1-183 <RES>

```

[illegible]

```
E:67-91/Domatin: leucine-rich alpha-2-glycoprotein repeat homolog <LRB>
E:32-434/Domatin: extracellular status predicted <EXT>
```

V



F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK2>  
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK3>  
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR3>  
 F:435-451/Domain: transmembrane #status predicted <TM>  
 F:452-821/Domain: cytosolic #status predicted <CYT>  
 F:535-813/Domain: protein kinase homology <KIN>  
 F:543-551/Region: protein kinase ATP-binding motif  
 F:571/Active site: Lys #status predicted  
 F:571/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
 F:816/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 13.2% Score 648.5; DB 1; Length 821;  
 Best Local Similarity 30.1%; Pred. No. 1.8e-22;  
 Matches 201; Conservative 72; Mismatches 188; Indels 207; Gaps 23;

QY 373 SPALGTPPPAPWPPPPPTNFSSLEPRGOOPAKAGSPPTAILGCLVALIILLLL 432  
 DB 217 SCVSGDDPLPTLYWDYGNLVSKHNNSTHOGSLRTINISSDSGKQISCY----- 267  
 QY 433 IALMLRLHWRLLSKAERNVLEELIYHLSV---PGDTILLNNRGPPEPP----- 482  
 DB 268 -----AENLVGEDDDSVNLTVHFAPTITFL-----ESPSTDHHC 302  
 QY 483 -PYOEDPRGNPPHSAFCVNGS-----ALLSNPA-----Y 513  
 DB 303 IFF---TVGNPKPALOWYFNGAILNESKICIKIHVTNTEYHGLQLOLNPMMNGDY 359  
 QY 514 RLIL-----ATYARPNGRGPPTPMAPKPTNTQAYSQDMEP--E 551  
 DB 360 TLMAKNKDEKDEROISAHFNGRPGVDYETNPNYPEVLIEDWTPTDI---GDTTNKSE 415  
 QY 552 KGGAPLPPPPQSVHYAEADIVTIGV----- 580  
 DB 416 IYSTVDADOTNRHLSVAVVAVVAVGCLLVMLLLKLARSKGKMGKPAVYSNDD 475  
 QY 581 -----TGNNTYAVPALPPGAVDGP---PRVDFP-----RS 608  
 DB 476 SASPLHINSNTPTSSSGGPDVAIIGMTKITVIENPOFGITNSOLKPDIVQHTKRH 535  
 QY 609 RLRFKKLEGGQGEVHLC---VDSPODVLSDPFLNVRKGPLLVAVKILRPDANKA 665  
 DB 536 NIVLKRLEGGAFKVFLEACYLCEPD-----KILVAVYTLK-DASDNA 580  
 QY 666 SPSLSRNFLEKVKIMSLKDPNIRLLGVCYQDDPLMTIDYMEGDIHQLSAQHE 755  
 DB 581 -----KDFHREAEELLTMOHEHIVKFGYGVCEGDPILINVEPKYMKHGDLNKLRAHGP 634  
 QY 726 D-KAAGAPGDDQAAGPT-ISTYMLHYAAOIASGMYLATLNFVHRDLATNCLVGEN 783  
 DB 635 AYLMAGNP-----PELTQSOMLHTAOQIAAGMYLASOHVHRDLATNCLVGEN 666  
 QY 784 FTIKIADFGMSNLVAGDYRYVQGAVALPIRMMAMECILMGKFTTASDVAFSVTLMEVL 843  
 DB 687 LLVKTIGDFGMSHDYVSTDYRVGHTMLPIRMMPEISIMYRKTTESDVMSGLGVMEIR 746  
 QY 844 MCRAPQFQQLDEQVYENAGFEFRQGRQVLSRPPAPQGLIYELMKCSSESQRPP 903  
 DB 747 TYGK-QPWFQLSNNEYIECI---TQGR-VLQRRTPCPQEVYELMLGCMQWRPEPTTRKN 798  
 QY 904 FSQLRHFL 911  
 DB 799 IKNIHTLL 806

RESULT 12  
 S44098  
 brain-derived neurotrophic factor receptor precursor - chicken  
 N:Alternate names: receptor tyrosine kinase trkB  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 11-Jun-1999

C:Accession: S59939; S42175; S44098  
 R:Vinh, N.O.; Erdmann, K.S.; Heumann, R.  
 Gene 149, 383-384, 1994  
 A:Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of  
 A:Reference number: S59938; MUID:95047511  
 A:Accession: S59939  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-818 <Y12>  
 A:Cross-references: EMBL:X77251; NID:9563881; PIDN:CAA54468.1; PID:9472934  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994  
 R:Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Potgiesser, J.; Barte, Y.A.  
 Development 119, 545-558, 1993  
 A:Title: Expression and binding characteristics of the BDNF receptor chick trkB.  
 A:Reference number: S42175; MUID:94116452  
 A:Accession: S42175  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-818 <DEC>  
 A:Cross-references: EMBL:X74109; NID:9407798; PIDN:CAA52210.1; PID:9407799  
 C:Genetics:  
 A:Gene: trkB  
 C:Function:  
 A:Description: regulation of nervous system development; receptor for brain-derived  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-gly  
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fac  
 inase  
 F:1-31/Domain: signal sequence #status predicted <SIG>  
 F:32-818/Product: brain-derived neurotrophic factor receptor #status predicted <MAY>  
 F:32-432/Domain: extracellular #status predicted <EX>  
 F:66-90/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
 F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
 F:115-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
 F:138-149/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
 F:433-449/Domain: transmembrane #status predicted <TM>  
 F:450-818/Domain: cytosolic #status predicted <CYT>  
 F:532-810/Domain: protein kinase homology <KIN>  
 F:540-548/Region: protein kinase ATP-binding motif  
 F:566,94,120,199,204,253,287,324,337,349,408/Binding site: carbohydrate (Asn) (coval  
 F:568/Active site: Lys #status predicted  
 F:702/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
 F:813/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 13.1% Score 648; DB 1; Length 818;  
 Best Local Similarity 34.2%; Pred. No. 1.9e-22;  
 Matches 176; Conservative 71; Mismatches 149; Indels 118; Gaps 19;

QY 446 LLSKAEERYVLEELIYH-LSVPDDTILLNNRPPPREPPPOE---PRPRGNPPH----- 495  
 DB 360 LLMKNEGGDEKRVDAHFMSVPGD-----GSGPIYDPDYVEETPNPDIGDTNNNSNOI 413  
 QY 496 SARPCEVNG-----SALLSNPARYLLATATARP-----RGGPPTPMAMP 537  
 DB 414 TSPDVNKNKEMEDSITYVVGIALVCTGLVIMLLIKGRHSGFKMGKPD----- 463  
 QY 538 TNYQVSGDIEMPEKPGAPLPPPPQNSVHYAEADIVTIGVGTNTYAVPALPPGAVG 597  
 DB 464 ---SSVISND-----DSDASPL-----HHNSGNSNTPSSSGGPDVAIIGMTKITPIV 507  
 QY 598 DGPPRVDFPRSRRL-----FKRKLEGGQGEVHLC---VDSPODVLSDP 640  
 DB 508 ENFOYFGITNSOLKPDPTVOHIKRNIIVLKRLEGGAFKVFLEACYLCEPD----- 561  
 QY 641 PLNVRKGHPLVAVKILRPDATKNAFSLSRNDPFEKVKIMSLKDPNIRLLGVCYQD 700  
 DB 562 -----KILVAVYTLK-DASDNA-----KDFHREAEELLTMOHEHIVKFGYGVCEG 606  
 QY 701 DPLCMITDYMENGLDQVLSAQHLEDKAAGAPGDDQAAG---PTISYMLHYAAQIA 757  
 DB 607 DPLIMFEYMKHGDLNKLFRH-----GPDVAVLMAGNRPPELLTQSOMLHTAOQIA 657  
 QY 758 SGRMYLATLNFVHRDLATNCLVGENFTIKIDFGMSRLVAGDYRYVQGAVALPIRMA 817





Db 593 TNLHEHIVKFEYGCDDPLIMVEYMKHGDILNKFLEAH-----GPNAMILVYDQ 643

QY 738 AAGP-TISYMLHVAQAISGMRYLATLNFVRDLATRNCLVGENFTIKIADFGSMRN 796

Db 644 PROAKGELGSLQMLHISQIASGVYLAHQFVHRDLATRNCLVGENFTIKIADFGSMRD 703

QY 797 LLAGDYRVAGRAVLPIRMAMECILMGKFTTASDVMAFVGLMEVLMCRAPPGQLT 856

Db 704 VYSDYRVAGRHMLPIRMAMECILMGKFTTASDVMAFVGLMEVLMCRAPPGQLT 762

QY 857 EGVENAGFEFFRDGROYVLSRPPACDGLYELMLRCMSRESEORPPESQLRFL 911

Db 763 TEVIECI-----TQGR--VLERPRVCPREYVDVLMGCGQRPPQRLNKEIKYL 810

RESULT 15

TVRRTB

nerve growth factor receptor precursor, high affinity - rat

N:Alternate names: receptor tyrosine kinase trka

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 02-Jun-2000

C:Accession: A41981

R:Weakli, S.O.; Suter, U.; Drinkwater, C.C.; Weischer, A.A.; Shooter, E.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 2374-2378, 1992

A:Title: The rat trk proto-oncogene product exhibits properties characteristic of the src

A:Reference number: A41981, M0ID:92186121

A:Accession: A41981

A:Molecule type: mRNA

A:Residues: 1-799 <MEAS>

A:Cross-reference: GB:M85214; NID:g207481; PIDN:AAA42286.1; PID:g207482

A:Note: sequence extracted from NCBI backbone (NCBI:88433, NCBI:88434)

C:Comment: In Genbank entry RATTNRKPEC, release 113.0, the source is designated as Rattus r

C:Function: The proto-oncogene trka is activated by gene fusion. The amino end of several

A:Description: regulation of nervous system development; receptor for nerve growth fact

C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop

C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote

C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote

F:1-33/Domain: signal sequence #status predicted <SIG>

F:33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>

F:33-424/Domain: extracellular #status predicted <EXT>

F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:425-441/Domain: transmembrane #status predicted <TMN>

F:442-799/Domain: cytosolic #status predicted <CYT>

F:511-791/Domain: protein kinase homology <KIN>

F:519-527/Region: protein kinase ATP-binding motif

F:67,121,190,204,255,264,320,325,341,361,404/Binding site: carbohydrate (Asn) (covalent)

F:547/Active site: Lys #status predicted

F:683/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

F:794/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 13.0%; Score 640.5; DB 1; Length 799;

Best Local Similarity 29.5%; Pred. No. 4e-22;

Matches 190; Conservative 78; Mismatches 155; Indels 221; Gaps 22;

QY 335 SVPLGGRVARFLQC-----RFLFAGPMLLFSEISFI----- 365

Db 289 SVHLGNAVEQHHMCIPFSVDGQAPAPSLRWFNGS--VLNETSFITQFLESALTNETMRH 346

QY 366 -----SDVNNSSPALGTFP-----PAPMPGPPPTNFSLEPR 403

Db 347 GCLRLNPTHTVNGNTLLAANPYGAASITAAAFMDNPFERFEDPIPVSSPVDNST 406

QY 404 GOOPVAKAEGSPTAILIGLVAIILLLIILMLRMLRRLSKERR-----V 454

Db 407 SRDPVEKDETPFGVSAVGLAVSALFL-SALLL-----VLNKGGRSKGIRNPAY 458

QY 455 LEEF-----LTVHLSPGCTILINRPPGPREPPPTQEPFRPNPNSADPCVNGSAL---L 507

Db 459 LAPEDGLAMSLHFMTLGSSSL-----SPEEGKSGSLQCHI 493

QY 508 LSNPAYRLLATYAPRPPGPPPTPAKAPNTQAVSSDYMEPEKPGAPLPPPPQNSVP 567

Db 494 MENPOY-----FS-----DTCVH 506

QY 568 HYAEADIVTLGGVGTNTYAAPALPPGAVGDPFRVDPFRSLRKEKELGSGGGEVHC 627

Db 507 HIKRODII-----LKMELGSGAGAKYFLA 530

QY 628 E---VDSQDLYSLDFPLNVRKGHPLVAVKILRPDARKNASFSLFSRNDLKEVKIMSR 684

Db 531 ECVNMLNDQ-----KMLVAVKALK-ETSENA-----KQDFHREALLTM 569

QY 685 LKDPRIIRLGVYODDPLCMITDYMENGDLNPLSAQLDRAEAPGQGOAAGPTI 744

Db 570 LQHQHIVAFEGVCTEGGFLMVFETMRHGDILNREFLRSHGPPAKLLAGE--DVAPGP-L 625

QY 745 SYPMILHVAQAISGMRYLATLNFVRDLATRNCLVGENFTIKIADFGSMRNLYAGDYR 804

Db 626 GLGQDLAVASQVAAQVYLAHQFVHRDLATRNCLVGENFTIKIADFGSMRDITSTYR 685

QY 805 VQGRAVLPIRMAMECILMGKFTTASDVMAFVGLMEVLMCRAPPGQLTDEQVIEAG 864

Db 686 VGGRTMPLPIRMAMECILMGKFTTASDVMAFVGLMEVLMCRAPPGQLTDEQVIEAG 743

QY 865 EFPDQGRVYLSRPPACDGLYELMLRCMSRESEORPPESQLRFL 908

Db 744 ----TQGR--LERPRACPPDVYALMGCGQRPPQRLNKEIKYL 781

Search completed: October 4, 2002, 07:41:35

Job time: 155 sec